

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2009; month=12; day=22; hr=7; min=36; sec=29; ms=626; ]

=====

Application No: 10575640 Version No: 2.0

Input Set:

Output Set:

Started: 2009-12-02 14:52:57.887  
Finished: 2009-12-02 14:52:59.820  
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 933 ms  
Total Warnings: 6  
Total Errors: 0  
No. of SeqIDs Defined: 66  
Actual SeqID Count: 66

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)

# SEQUENCE LISTING

<110> TURECI, Ozlem  
SAHIN, Ugar  
KREITER, Sebastian

<120> Recombinant Vaccines and Use Thereof

<130> VOS-120

<140> 10575640

<141> 2009-12-02

<150> PCT/EP2004/011512

<151> 2004-10-13

<150> DE 103 47 710.1

<151> 2003-10-14

<160> 66

<170> PatentIn version 3.1

<210> 1

<211> 78

<212> DNA

<213> Homo sapiens

<400> 1

atgcgggtca cggcgcccg aaccctcatc ctgctgctct cgggagccct ggcctgacc 60

gagacctggg cgggtcc 78

<210> 2

<211> 26

<212> PRT

<213> Homo sapiens

<400> 2

Met Arg Val Thr Ala Pro Arg Thr Leu Ile Leu Leu Leu Ser Gly Ala

1 5 10 15

Leu Ala Leu Thr Glu Thr Trp Ala Gly Ser

20 25

<210> 3

<211> 168

<212> DNA

<213> Homo sapiens

<400> 3

atcgtgggca ttgttgctgg cctggctgtc ctagcagttg tggcatcgg agctgtggtc 60

gctactgtga tgtgtaggag gaagagctca ggtggaaaag gagggagcta ctctcaggct 120

gcgtccagcg acagtgccca gggctctgat gtgtctctca cagcttga 168

<210> 4  
<211> 55  
<212> PRT  
<213> Homo sapiens

<400> 4

Ile Val Gly Ile Val Ala Gly Leu Ala Val Leu Ala Val Val Val Ile  
1 5 10 15

Gly Ala Val Val Ala Thr Val Met Cys Arg Arg Lys Ser Ser Gly Gly  
20 25 30

Lys Gly Gly Ser Tyr Ser Gln Ala Ala Ser Ser Asp Ser Ala Gln Gly  
35 40 45

Ser Asp Val Ser Leu Thr Ala  
50 55

<210> 5  
<211> 129  
<212> DNA  
<213> Homo sapiens

<400> 5  
cagagcaaga tgctgagtgg agtcgggggc tttgtgctgg gcctgctctt ccttggggcc 60

gggctgttca tctacttcag gaatcagaaa ggacactctg gacttcagcc aagaggattc 120

ctgagctga 129

<210> 6  
<211> 42  
<212> PRT  
<213> Homo sapiens

<400> 6

Gln Ser Lys Met Leu Ser Gly Val Gly Gly Phe Val Leu Gly Leu Leu  
1 5 10 15

Phe Leu Gly Ala Gly Leu Phe Ile Tyr Phe Arg Asn Gln Lys Gly His  
20 25 30

Ser Gly Leu Gln Pro Arg Gly Phe Leu Ser  
35 40

<210> 7  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> DNA of restriction site in human HLA class I domains

<400> 7  
ctgcaggtcg actctagagg atcc 24

<210> 8  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Restriction site in human HLA class I domains

<400> 8

Leu Gln Val Asp Ser Arg Gly Ser  
1 5

<210> 9  
<211> 1683  
<212> DNA  
<213> Human cytomegalovirus

<400> 9  
atggagtcgc gcggtcgccg ttgtcccgaa atgatatccg tactgggtcc catttcgggg 60  
cacgtgctga aagccgtgtt tagtcgcggc gatacgccgg tgctgccgca cgagacgcga 120  
ctcctgcaga cgggtatcca cgtacgcgtg agccagccct cgctgatctt ggtatcgcag 180  
tacacgcccg actcgacgcc atgccaccgc ggcgacaatc agctgcaggt gcagcacacg 240  
tactttacgg gcagcgaggt ggagaacgtg tcggtcaacg tgcacaaccc cacgggccga 300  
agcatctgcc ccagccagga gcccatgtcg atctatgtgt acgcgctgcc gctcaagatg 360  
ctgaacatcc ccagcatcaa cgtgcaccac taccgcgtcg cggccgagcg caaacaccga 420  
cacctgcccg tagctgacgc tgtgattcac gcgtcgggca agcagatgtg gcaggcgcgt 480  
ctcacggtct cgggactggc ctggacgcgt cagcagaacc agtggaaaga gcccgacgtc 540  
tactacacgt cagcgttcgt gtttcccacc aaggacgtgg cactgcggca cgtggtgtgc 600  
gcgcacgagc tggtttgctc catggagaac acgcgcgcaa ccaagatgca ggtgataggt 660

gaccagtacg tcaaggtgta cctggagtcc ttctgcgagg acgtgccctc cggcaagctc	720
tttatgcacg tcacgctggg ctctgacgtg gaagaggacc tgacgatgac ccgcaaccgg	780
caacccttca tgcgccccca cgagcgcgaac ggcttttacgg tgttgtgtcc caaaaatatg	840
ataatcaaac cgggcaagat ctgcgcacatc atgctggatg tggtcttttac ctcacacgag	900
cattttgggc tgctgtgtcc caagagcatc ccgggcctga gcattctcagg taacctgttg	960
atgaacgggc agcagatctt cctggaggta caagccatac gcgagaccgt ggaactgcgt	1020
cagtacgatc ccgtggctgc gctcttcttt ttcgatatcg acttgctgct gcagcgcggg	1080
cctcagtaca gcgagcacc cacccttcacc agccagtatc gcattccagg caagcttgag	1140
taccgacaca cctgggaccg gcacgacgag ggtgccgccc agggcgacga cgacgtctgg	1200
accagcggat cggactccga cgaagaactc gtaaccaccg agcgcaagac gccccgcgtc	1260
accggcggcg gcgccatggc gggcgcctcc acttccgcgg gccgcaaacg caaatcagca	1320
tcctcggcga cggcgtgcac gtcgggcgtt atgacacgcg gccgccttaa ggccgagtcc	1380
accgtcgcgc ccgaagagga caccgacgag gattccgaca acgaaatcca caatccggcc	1440
gtgttcacct ggccgccttg gcaggccggc atcctggccc gcaacctggt gcccatggtg	1500
gtacggttc agggtcagaa tctgaagtac caggaattct tctgggacgc caacgacatc	1560
taccgcatct tcgccgaatt ggaaggcgta tggcagcccg ctgcgcaacc caaacgtcgc	1620
cgccaccggc aagacgcctt gcccgggcca tgcategect cgacgcccga aaagcaccga	1680
ggt	1683

<210> 10

<211> 561

<212> PRT

<213> Human cytomegalovirus

<400> 10

Met	Glu	Ser	Arg	Gly	Arg	Arg	Cys	Pro	Glu	Met	Ile	Ser	Val	Leu	Gly
1				5				10						15	

Pro	Ile	Ser	Gly	His	Val	Leu	Lys	Ala	Val	Phe	Ser	Arg	Gly	Asp	Thr
			20					25					30		

Pro	Val	Leu	Pro	His	Glu	Thr	Arg	Leu	Leu	Gln	Thr	Gly	Ile	His	Val
		35						40				45			

Arg Val Ser Gln Pro Ser Leu Ile Leu Val Ser Gln Tyr Thr Pro Asp  
50 55 60

Ser Thr Pro Cys His Arg Gly Asp Asn Gln Leu Gln Val Gln His Thr  
65 70 75 80

Tyr Phe Thr Gly Ser Glu Val Glu Asn Val Ser Val Asn Val His Asn  
85 90 95

Pro Thr Gly Arg Ser Ile Cys Pro Ser Gln Glu Pro Met Ser Ile Tyr  
100 105 110

Val Tyr Ala Leu Pro Leu Lys Met Leu Asn Ile Pro Ser Ile Asn Val  
115 120 125

His His Tyr Pro Ser Ala Ala Glu Arg Lys His Arg His Leu Pro Val  
130 135 140

Ala Asp Ala Val Ile His Ala Ser Gly Lys Gln Met Trp Gln Ala Arg  
145 150 155 160

Leu Thr Val Ser Gly Leu Ala Trp Thr Arg Gln Gln Asn Gln Trp Lys  
165 170 175

Glu Pro Asp Val Tyr Tyr Thr Ser Ala Phe Val Phe Pro Thr Lys Asp  
180 185 190

Val Ala Leu Arg His Val Val Cys Ala His Glu Leu Val Cys Ser Met  
195 200 205

Glu Asn Thr Arg Ala Thr Lys Met Gln Val Ile Gly Asp Gln Tyr Val  
210 215 220

Lys Val Tyr Leu Glu Ser Phe Cys Glu Asp Val Pro Ser Gly Lys Leu  
225 230 235 240

Phe Met His Val Thr Leu Gly Ser Asp Val Glu Glu Asp Leu Thr Met  
245 250 255

Thr Arg Asn Pro Gln Pro Phe Met Arg Pro His Glu Arg Asn Gly Phe  
260 265 270

Thr Val Leu Cys Pro Lys Asn Met Ile Ile Lys Pro Gly Lys Ile Ser

275

280

285

His Ile Met Leu Asp Val Ala Phe Thr Ser His Glu His Phe Gly Leu  
290 295 300

Leu Cys Pro Lys Ser Ile Pro Gly Leu Ser Ile Ser Gly Asn Leu Leu  
305 310 315 320

Met Asn Gly Gln Gln Ile Phe Leu Glu Val Gln Ala Ile Arg Glu Thr  
325 330 335

Val Glu Leu Arg Gln Tyr Asp Pro Val Ala Ala Leu Phe Phe Phe Asp  
340 345 350

Ile Asp Leu Leu Leu Gln Arg Gly Pro Gln Tyr Ser Glu His Pro Thr  
355 360 365

Phe Thr Ser Gln Tyr Arg Ile Gln Gly Lys Leu Glu Tyr Arg His Thr  
370 375 380

Trp Asp Arg His Asp Glu Gly Ala Ala Gln Gly Asp Asp Asp Val Trp  
385 390 395 400

Thr Ser Gly Ser Asp Ser Asp Glu Glu Leu Val Thr Thr Glu Arg Lys  
405 410 415

Thr Pro Arg Val Thr Gly Gly Gly Ala Met Ala Gly Ala Ser Thr Ser  
420 425 430

Ala Gly Arg Lys Arg Lys Ser Ala Ser Ser Ala Thr Ala Cys Thr Ser  
435 440 445

Gly Val Met Thr Arg Gly Arg Leu Lys Ala Glu Ser Thr Val Ala Pro  
450 455 460

Glu Glu Asp Thr Asp Glu Asp Ser Asp Asn Glu Ile His Asn Pro Ala  
465 470 475 480

Val Phe Thr Trp Pro Pro Trp Gln Ala Gly Ile Leu Ala Arg Asn Leu  
485 490 495

Val Pro Met Val Ala Thr Val Gln Gly Gln Asn Leu Lys Tyr Gln Glu  
500 505 510



Phe Phe Trp Asp Ala Asn Asp Ile Tyr Arg Ile Phe Ala Glu Leu Glu  
515 520 525

Gly Val Trp Gln Pro Ala Ala Gln Pro Lys Arg Arg Arg His Arg Gln  
530 535 540

Asp Ala Leu Pro Gly Pro Cys Ile Ala Ser Thr Pro Lys Lys His Arg  
545 550 555 560

Gly

<210> 11

<211> 1962

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding human HLA class I domains and CMV pp65

<400> 11

atgcggggtca cggcgcccccg aaccctcatc ctgctgctct cgggagccct ggccctgacc	60
gagacctggg ccggctccct gcaggtcgac tctagaggat ccaccatgga gtcgcgcggt	120
cgccgttggtc ccgaaatgat atccgtactg ggtcccattt cggggcacgt gctgaaagcc	180
gtgttttagtc gggcgatac gccgggtgctg ccgcacgaga cgcgactcct gcagacgggt	240
atccacgtac gcgtagacca gccctcgctg atcttggtat cgcagtacac gcccgactcg	300
acgccatgcc accgcggcga caatcagctg caggtgcagc acacgtactt tacgggcagc	360
gaggtggaga acgtgtcggg caacgtgcac aacccacgg gccgaagcat ctgcccagc	420
caggagccca tgtcgatcta tgtgtacgag ctgccgctca agatgctgaa catccccagc	480
atcaacgtgc accactaccc gtcggcgggc gagcgcaaac accgacacct gcccgtagct	540
gacgctgtga ttcacgcgtc gggcaagcag atgtggcagg cgcgtctcac ggtctcggga	600
ctggcctgga cgcgtcagca gaaccagtgg aaagagcccg acgtctacta cacgtcagcg	660
ttcgtgtttc ccaccaagga cgtggcactg cggcacgtgg tgtgcgcgca cgagctggtt	720
tgctccatgg agaacacgag cgcaaccaag atgcaggtga taggtgacca gtacgtcaag	780
gtgtacctgg agtccttctg cgaggacgtg ccctccggca agctctttat gcacgtcacg	840
ctgggctctg acgtggaaga ggacctgacg atgaccgcga acccgcaacc cttcatgcgc	900

```

ccccacgagc gcaacggcctt tacggtgttg tgtcccaaaa atatgataat caaacccgggc 960
aagatctcgc acatcatgct ggatgtggct ttacctcac acgagcattt tgggctgctg 1020
tgtcccaaga gcatcccggt cctgagcatc tcaggtaacc tgttgatgaa cgggcagcag 1080
atcttctctg aggtacaagc catacgcgag accgtggaac tgcgtcagta cgatcccggt 1140
gctgcgctct tctttttcga tatcgacttg ctgctgcagc gcgggcctca gtacagcgag 1200
caccacacct tcaccagcca gtatcgcatc cagggaagc ttgagtaccg acacacctgg 1260
gaccggcacg acgaggggtg cggccagggc gacgacgacg tctggaccag cggatcggac 1320
tccgacgaag aactcgtaac caccgagcgc aagacgcccc gcgtcaccgg cggcggcgcc 1380
atggcgggcg cctccacttc cgcggggcgc aaacgcaa atcagcatctc ggcgacggcg 1440
tgcacgtcgg gcgttatgac acgcggcgcg cttaaggccg agtccaccgt cgcgcccga 1500
gaggacaccg acgaggattc cgacaacgaa atccacaatc cggccgtgtt cacctggccg 1560
ccctggcagg cgggcatact ggcccgaac ctggtgccca tgggtggctac ggttcagggt 1620
cagaatctga agtaccagga attcttcttg gacgccaacg acatctaccg catcttcgcc 1680
gaattggaag gcgtatggca gcccgctgcg caacccaaac gtcgccgcca ccggcaagac 1740
gccttgcccc ggccatgcat cgcctcgacg cccaaaagc accgaggtgg atccatcgtg 1800
ggcattgttg ctggcctggc tgtcctagca gttgtggtca tcggagctgt ggtcgctact 1860
gtgatgtgta ggaggaagag ctcaggtgga aaaggaggga gctactctca ggctgcgtcc 1920
agcgacagtg cccagggtc tgatgtgtct ctacagctt ga 1962

```

<210> 12

<211> 653

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion protein of human HLA class I domains and CMV pp65

<400> 12

```

Met Arg Val Thr Ala Pro Arg Thr Leu Ile Leu Leu Leu Ser Gly Ala
1           5           10          15

```

```

Leu Ala Leu Thr Glu Thr Trp Ala Gly Ser Leu Gln Val Asp Ser Arg
          20           25           30

```

```

Gly Ser Thr Met Glu Ser Arg Gly Arg Arg Cys Pro Glu Met Ile Ser
          35           40           45

```

Val Leu Gly Pro Ile Ser Gly His Val Leu Lys Ala Val Phe Ser Arg  
50 55 60

Gly Asp Thr Pro Val Leu Pro His Glu Thr Arg Leu Leu Gln Thr Gly  
65 70 75 80

Ile His Val Arg Val Ser Gln Pro Ser Leu Ile Leu Val Ser Gln Tyr  
85 90 95

Thr Pro Asp Ser Thr Pro Cys His Arg Gly Asp Asn Gln Leu Gln Val  
100 105 110

Gln His Thr Tyr Phe Thr Gly Ser Glu Val Glu Asn Val Ser Val Asn  
115 120 125

Val His Asn Pro Thr Gly Arg Ser Ile Cys Pro Ser Gln Glu Pro Met  
130 135 140

Ser Ile Tyr Val Tyr Ala Leu Pro Leu Lys Met Leu Asn Ile Pro Ser  
145 150 155 160

Ile Asn Val His His Tyr Pro Ser Ala Ala Glu Arg Lys His Arg His  
165 170 175

Leu Pro Val Ala Asp Ala Val Ile His Ala Ser Gly Lys Gln Met Trp  
180 185 190

Gln Ala Arg Leu Thr Val Ser Gly Leu Ala Trp Thr Arg Gln Gln Asn  
195 200 205

Gln Trp Lys Glu Pro Asp Val Tyr Tyr Thr Ser Ala Phe Val Phe Pro  
210 215 220

Thr Lys Asp Val Ala Leu Arg His Val Val Cys Ala His Glu Leu Val  
225 230 235 240

Cys Ser Met Glu Asn Thr Arg Ala Thr Lys Met Gln Val Ile Gly Asp  
245 250 255

Gln Tyr Val Lys Val Tyr Leu Glu Ser Phe Cys Glu Asp Val Pro Ser  
260 265 270

Gly	Lys	Leu	Phe	Met	His	Val	Thr	Leu	Gly	Ser	Asp	Val	Glu	Glu	Asp	275	280	285
Leu	Thr	Met	Thr	Arg	Asn	Pro	Gln	Pro	Phe	Met	Arg	Pro	His	Glu	Arg	290	295	300
Asn	Gly	Phe	Thr	Val	Leu	Cys	Pro	Lys	Asn	Met	Ile	Ile	Lys	Pro	Gly	305	310	315
Lys	Ile	Ser	His	Ile	Met	Leu	Asp	Val	Ala	Phe	Thr	Ser	His	Glu	His	325	330	335
Phe	Gly	Leu	Leu	Cys	Pro	Lys	Ser	Ile	Pro	Gly	Leu	Ser	Ile	Ser	Gly	340	345	350
Asn	Leu	Leu	Met	Asn	Gly	Gln	Gln	Ile	Phe	Leu	Glu	Val	Gln	Ala	Ile	355	360	365
Arg	Glu	Thr	Val	Glu	Leu	Arg	Gln	Tyr	Asp	Pro	Val	Ala	Ala	Leu	Phe	370	375	380
Phe	Phe	Asp	Ile	Asp	Leu	Leu	Leu	Gln	Arg	Gly	Pro	Gln	Tyr	Ser	Glu	385	390	395
His	Pro	Thr	Phe	Thr	Ser	Gln	Tyr	Arg	Ile	Gln	Gly	Lys	Leu	Glu	Tyr	405	410	415
Arg	His	Thr	Trp	Asp	Arg	His	Asp	Glu	Gly	Ala	Ala	Gln	Gly	Asp	Asp	420	425	430
Asp	Val	Trp	Thr	Ser	Gly	Ser	Asp	Ser	Asp	Glu	Glu	Leu	Val	Thr	Thr	435	440	445
Glu	Arg	Lys	Thr	Pro	Arg	Val	Thr	Gly	Gly	Gly	Ala	Met	Ala	Gly	Ala	450	455	460
Ser	Thr	Ser	Ala	Gly	Arg	Lys	Arg	Lys	Ser	Ala	Ser	Ser	Ala	Thr	Ala	465	470	475
Cys	Thr	Ser	Gly	Val	Met	Thr	Arg	Gly	Arg	Leu	Lys	Ala	Glu	Ser	Thr	485	490	495

Val Ala Pro Glu Glu Asp Thr Asp Glu Asp Ser Asp Asn Glu Ile His  
500 505 510

Asn Pro Ala Val Phe Thr Trp Pro Pro Trp Gln Ala Gly Ile Leu Ala  
515 520 525

Arg Asn Leu Val Pro Met Val Ala Thr Val Gln Gly Gln Asn Leu Lys  
530 535 540

Tyr Gln Glu Phe Phe Trp Asp Ala Asn Asp Ile Tyr Arg Ile Phe Ala  
545 550 555 560

Glu Leu Glu Gly Val Trp Gln Pro Ala Ala Gln Pro Lys Arg Arg Arg  
565 570 575

His Arg Gln Asp Ala Leu Pro Gly Pro Cys Ile Ala Ser Thr Pro L